STIC-Biotech/ChemLib

From: Sent:

Kemmerer, Elizabeth Monday, September 22, 2003 3:40 PM STIC-Biotech/ChemLib seq search req

To:

Subject:

Please search SEQ ID NO: 2 for 10/004832.

Thanks, '

Elizabeth (Betsy) Kemmerer Art Unit 1646 308-2673 CM1-10B17 Mailbox: 10D19

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:

/ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Copyright (c) 1993 - 2003 Compus
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AAY39813
AAB21089
AAY54900
AAE14612
ABG74162
AAB58304
AAR43941
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                                                                              Haematopoietic mat
CBFBOEII protein s
Human CBFBOEII pro
Human haemopoietic
Human haemopoietic
                                                                                                                                                                                                          Description
Lung cancer associ
Human Glia Maturat
Novel human diagno
                                                                 Human haemopoietic
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	AAG47863	21	132	14.1	104	45
	7	21	132	14.1	104	44
Arabidopsis thalia	AAG47844	21	178	14.3	105	43
	AAG11684	21	139	14.3	105	42
	AAG47845	21	132	14.3	105	41
thali	83	21	132	14.3	105	40
	AAU09098	22	348	14.7	108	39
	AAG04372	21	150	14.7	108	38
	AAG10070	21	139	14.7	108	37
	AAG05740	21	139	14.7	108	36
	AAG10071	21	132	14.7	108	ω 5
	AAG05741	21	132	14.7	108	34
	AAG04373	21	132	14.7	108	ω ω
Human protein SEQ	AAM79926	22	399	•	109	3 2
paB conti	AAY22216	20	351	•	109	31
Novel protein kina	AAB65617	22	349	•	109	30
Human protein SEQ	AAM78942	22	349	•	109	29
=	ABB59681	22	343		109.5	28
Arabidopsis thalia	AAG41987	21	170	•	111.5	27
thali	AAG41988	21	140	•	111.5	26
	AAG05222	21	140	•	111.5	. 25
	AAG41989	21	133	•	111.5	24
	AAG37448	21	133	•	111.5	23
	AAG05223	21	133	•	111.5	22
colon	AAG73824	22	385		113	21
വ	AAB53426	21	385	•	113	20
Human ovarian canc	ABG96404	23	350	•	113	19
Deduced human prot	AAR76598	16	350	•	113	18
	AAR43949	14	27	•	148	17
Human DITHP growth	ABR41794	24	113	•	154	16
. human	ABG19925	22	46	•	167	15
Novel human diagno	ABG19924	22	58	•	247.5	14
Drosophila melanog	ABB61879	22	141	•	376	13
Human secreted pro	0395	21	116	•	464.5	12
	99	22	126	69.9	513.5	11
Human secreted pro	AAY36208	20	109	•	558	10

ALIGNMENTS

RESULT 1 AAR81309 ID AAR8 New DNA encoding human haemopoietic maturation factor - useful in treatment and diagnosis, e.g. of cancer, leukaemia, haemophilia etc Adams 25-JAN-1994; 10-MAY-1994; 27-JUL-1995 W09519985-A1 Homo sapiens Hematopoietic Haematopoietic maturation factor 22-DEC-1995 AAR81309; AAR81309 standard; Protein; (HUMA-) HUMAN GENOME SCI INC 1995-269411/35 DB; AAQ99843. MD, Kirkness E, (first maturation factor; cancer; leukemia; hemophilia. 94US-0187186. 94WO-US05186 Olsen H, 142 AA. Rosen C

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RESULT 2
AAY39813
ID AAY3
AAY39813
AX AAY39813
AX AAY3
AX AAY3
AX CAPE
XX CAPE
XX CAPE
XX NO
CAPE
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Best Local Sim.
Matches 142;
                                         This sequence represents the human CBFBOE11 protein of the invention. CBFBOE11 is homologous to glia maturation factor beta. The CBFBOE11 coding sequence, vectors containing it and recombinant host cells are useful for recombinant production of CBFBOE11. The CBFBOE11 DNA, protein, and antibodies against CBFBOE11 are useful as research reagents, for screening assays and in diagnostic assays. Antagonists and agonists of CBFBOE11 can be used to inhibit or enhance, respectively, the activity of CBFBOE11 or expression of the DNA. Anti-CBFBOE11 antibodies and CBFBOE11 or inhibit or enhance, respectively, the activity of CBFBOE11 or expression of the DNA. Anti-CBFBOE11 antibodies and CBFBOE11 or its fragments can be used in vaccines. In particular, the proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                         Claim 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CBFBOEll; glia maturation factor beta; vaccine; neurological disease; autoimmune disease.
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                           agonists and antagonists can be used for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
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Pred. No. 6.7e-74;
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  autoimmune
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such as cancer, neurological disease, and autoimmune disease. The
CBFBOEll proteins and nucleotides may also be used in the diagnos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                        This sequence represents human CBFBOE11 protein. CBFBOE11 is a homologue of neuroglla mature factor beta (GMF-beta). The invention also encompasses the recombinant production of CBFBOE11 protein. The invention additionally relates to methods of utilising BFBOE11 protein the production additionally relates to methods of utilising BFBOE11 protein the protein additionally relates to methods of utilising BFBOE11 protein the protein additionally relates to methods of utilising BFBOE11 proteins and the protein and the protein additionally relates to methods of utilising BFBOE11 protein and the protein additionally relates to methods of utilising BFBOE11 protein and the protein additionally relates to methods of utilising BFBOE11 protein and the protein additional protein and the protein additional protein and the protein additional protein add
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human neuroglia mature factor (GMF)
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ilarity 100.0%;
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Score 735; I
Pred. No. 6.7
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Pred. No. 6.7e-74;
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                                                                                                                                                                                                                                                                             the invention. The HMF polypeptide is capable of inhibiting leukaemia cell proliferation, stimulating T-cell proliferation and differentiation, stimulating thymocyte proliferation and stimulating haematopoletic progenitor cell formation. HMF is useful for treating leukaemia and other blood disorders, e.g. haemolysis, polycythaemia vera, melogibrosis, haemophilia and splenomegaly, and for inducing differentiation of immature malignant leukaemia cells. HMF has a narrower range of activities and greater specificity for functionally differentiated cells than general growth factors and so can be used to treat diseases specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemopoietic maturation factor polypeptide useful for inhibiting leukaemia cell proliferation, stimulating T-cell proliferation and differentiation, stimulating thymocyte proliferation and stimulating haemopoietic progenitor cell formation -
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                                                                                                                                              ll Similarity
142; Conser
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                      LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                                                                               MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
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                                                                                                                                            0;
                                                                                                                                       Score 735; DB 21;
Pred. No. 6.7e-74;
: Mismatches 0;
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                                                                                                                                                                               Length 142;
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RESULT 5
AAE14612
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                                                                                                                                                Query Match
Best Local S
Matches 142
                                                                                                                                                                                                                                                       The invention relates to an antibody that specifically binds to human haemopoletic maturation factor (HMF). The antibody is useful as antagonist of HMF polypeptide, to prevent expansion of T cells which me be employed for treating conditions related to the presence of T cells e.g. graft rejection and autoimmune diseases. The antibody is also useful to isolate HMF polypeptide from tissue expressing the polypeptide, and in diagnostic assays for detecting altered levels of the polypeptide in various tissues. The HMF polypeptide and polynucleotide are utilised for therapeutic purposes, e.g. to treat leukaemia, blood-related disorders (e.g. haemolysis, haemophilia, splenomegaly), to stimulate differentiation and proliferation of cells haematopoietic or stromal origin, and to remove malignant cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1;
                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody that specifically binds to factor polypeptide, useful to prevent T graft rejection and autoimmune diseases
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25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1999;
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                                                                                                                                                  al Similarity
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                                                                        MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDROMVVLEEEFQNISPEELKME
EF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEIRTTDDLTEAWLQEKLSFFR
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                                                                                                                                                                                                                          142 AA;
                                                                                                                                                  Conservative
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94US-0187186
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                                                                                                                                                  0;
                                                                                                                                                Score 735; DB 23; Pred. No. 6.7e-74; Mismatches 0;
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blood-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,SH
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RESULT 6
ABG74162
ID ABG74162
XX ABG7

                          CC polypeptide and a host cell genetically engineered with the polypeptide of the collection (ATCC) (MMF.)

CC polypeptide and a host cell genetically engineered with the polypeptide care useful for identifying compounds active as agonists or antagonists to collection (ATCC) (MMF.)

CC HMF. The nucleic acid encoding the polypeptide is useful for diagnosing a collection of the collection of collection and the collection of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated hemopoletic maturation factor polypeptide useful stimulating hemopolesis, for treating leukemia, anemia, thrombocytopenia, and granulocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 16; Fig 1; 27pp; English.
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15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-DEC-2001;
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haematopoietic cell precursor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to an isolated haemopoietic maturation factor
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l precursor replacement; bone marrow transplant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
```

(HMF)

stimulation

of.

marrow recovery

due

Polynucleotide sequences AAF17982 - AAF18424 encode human lung ca associated proteins represented in AAB58106 - AAB58548. Lung canc associated proteins and polynucleotide sequences, their agonists,

have neuroprotective;

cytostatic;

Claim

1140-1141;

1425pp;

English.

```
RESULT 7
AAB58304
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       888888888x&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chemotherapy, for stimulating proliferation and differentiation of certain human T cell populations. The nucleic acid is useful as a prob for a cDNA library to isolate other genes which have high sequence similarity to the HMF gene or other similar biological activity and fo chromosomal identification. A compound which inhibits the polypeptide useful for preventing expansion of T cell populations, for treating conditions such as graft rejection and autoimmune diseases. The present sequence represents the amino acid sequence of human haemopoietic
                                                                                                                                                                                                                                                                                                                                       cardioactive; immunomodulatory; muscular active; v gastrointestinal; nephrotropic; antiinfective; gyr antibacterial; diagnosis; neural disorder; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            maturation factor.
                                                                                                  Lung
                                                                                                                                                                                (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB58304
                                                                                                                          N-PSDB;
                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                       08-MAR-2000;
                                                                                                                                                                                                                                                             21-SEP-2000
                                                                                                                                                                                                                                                                                  WO200055180-A2
                                                                                                                                                                                                                                                                                                                             proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                         gens,
                                                                                     cancer associated gene sequences, refergens, useful for treatment, prevention,
                                                                                                                        2000-587514/55
DB; AAF18180.
                                                                            as
                                                                                                                                                                                                                                                                                                                                                                                            cancer associated polypeptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
142; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                       lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ш
                                                                                                                                                                                HUMAN GENOME
ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSDSLYVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDROMVVLEEEFQNISPEELKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEIRTTDDLTEAWLQEKLSFFR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEIRTTDDLTEAWLQEKLSFFR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative
                                                                             cancer
                                                                                                                                                                                                                                       2000WO-US05918.
                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                             disorder;
                                                                                                                                                                                                                99US-0124270.
                                                                                                                                                                                                                                                                                                                                                                        associated
                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                           SCI INC
                                                                                                                                                                                                                                                                                                                             wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 735; DB 24;
Pred. No. 6.7e-74;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                             healing;
                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                         referred
tion, and
                                                                                                                                                                                                                                                                                                                                                                        neuroprotective;
                                                                                                                                                                                                                                                                                                                            infectious
                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                 gynecological;
                                                                                      to as lung cancer diagnosis of disorders
                                                                                                                                                                                                                                                                                                                                                                                               Ħ
                                                                                                                                                                                                                                                                                                                                                              vulnerary;
                                                                                                                                                                                                                                                                                                                             disease.
                                                                                                                                                                                                                                                                                                                                       disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                               642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     haemopoietic
                                                                                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
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RESULT 8
AAR43941
ID AAR4
XX AAR4
XX AAR4
XX AAR4
XX AAR4
XX GAF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                         28-NOV-1988;
26-APR-1991;
31-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulatory; muscular active general; vulnerary; gastrointestinal general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous othe diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                    , 14-DEC-1993
 N-PSDB; AAQ53862
                  WPI; 1993-405019/50
                                                      Jaye
                                                                                       (RHON )
                                                                                                                                                                                                                  31-OCT-1991;
                                                                                                                                                                                                                                                                                       US5270452-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Glia Maturation Factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
10-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR43941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR43941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences.
                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                      ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neuron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       factor
                                                                                     RHONE
UNIV 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQP
                                                    Kaplan R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDLTEAWLQEKLSFFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDLTEAWLQEKLSFFR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKXEQQMMYAGSKNRLVQTAELTKVFEIRTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     glial cell; nervous
                                                                                     POULENC RORER IOWA STATE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                         88US-0276847.
91US-0692772.
91US-0785185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                  91US-0785185
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 15..155
                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                      Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.1%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                              GME
                                                      ₽,
                                                                                                                                                                                                                                                                                                                         initiation codon"
                                                                                                                                                                                                                                                                                                                                          Met(14) corresponds to
                                                                                       FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system; regeneration; brain tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 699; DB 21; L
1. No. 7.3e-70;
1. hos 1;
                                                                                                        INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numerous other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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RESULT 9
ABG19927
ID ABG1
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Best Local S
Matches 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The human GMF sequence was deduced from a cDNA sequence obtained by screening a human brain stem library with a probe based on a bovine GMF tryptic fragment. Assuming that translation of GMF mRNA is initiated at the first ATG codon (see Features Table), the deduce protein is calculated to have a mol.wt. of 16716. GMF may be useful to treat injuries to the brain, spinal cord and nerves, to treat abnormal development of the nervous system and to arrest or reverse nervous system degeneration and the progress of tumours. (Updated on 25-MAR-2003 to correct PA field.)
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant glia maturation factbr useful for treating abnormal development of the nervous system - is obtd. by expression of cDNA obtd. from a human brain stem cDNA library using transformed
                                                                                                   N-PSDB;
                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                          31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                       30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABG19927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 7; 12pp; English.
                                                                                                                                                                                                       (HYSE-) HYSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG19927
                                                                                                     2001-639362/73.
)B; AAS84114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein; 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEIRTTDDLTEAWLQEKLSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEIRNTEDLTEEWLREKLGFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSESLVVCDVAEDLVEKLRKFRFAKETNNAAIIMKIDKDKRLVVLDEELEGISPDELKDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                       2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                             2000US-0540217
2000US-0649167
                                                                                                                                                                                                       INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.8%;
81.6%;
                                                                                                                                                                Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein #19918.
                                                                                                                                                                TY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 616; DB 14;
Pred. No. 1.4e-60;
5; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the deduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 10
AAY36208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC aliagong of sites expressing (II). (I) and (II) are useful for treating CC responsible for genetic disorders or other traits to assess biodiversity responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed sepecification, but was obtained in electronic format directly from WIPO at the wino internal contacts.
                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Sim
Matches 122;
                        04-SEP-1998;
13-NOV-1997;
17-DEC-1997;
09-FEB-1998;
13-APR-1998;
10-AUG-1998;
                                                                                                                                                                                                                                   Secreted protein; diagnostic; gene t
                                                                                                                         13-NOV-1998;
                                                                                                                                                    27-MAY-1999
                                                                                                                                                                               W09925825-A2
                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                             Human secreted
                                                                                                                                                                                                                                                                                                         23-SEP-1999
                                                                                                                                                                                                                                                                                                                                      AAY36208
                                                                                                                                                                                                                                                                                                                                                                AAY36208 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKVFEIRTTDDLT--EAWLQEKLSF 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDR-QMVVLEEEFQNISPE-ELKM
                                                                                                                                                                                                                                                                                                                                                                                                                                     TKGVPKSRTTXLTSLRPWLQEKLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRGQMVVLEEEFQNISPQRELKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID No 50286; 103pp; English.
                        98US-0099273.
97US-0066677.
97US-0069957.
98US-0074121.
98US-0081563.
98US-0096116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                             protein
                                                                                                                         98WO-IB01862
                                                                                                                                                                                                                                      human; cytostatic;
therapy; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.6%;
84.1%;
                                                                                                                                                                                                                                                                             #80
                                                                                                                                                                                                                                                                                                                                                                  109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 570; DB 22;
Pred. No. 2.3e-55;
2; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                A
                                                                                                                                                                                                                                   mapping;
                                                                                                                                                                                                                                                  thrombotic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                      secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
                                                                                                                                                                                                                                                  forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144
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RESULT 11
ABG19926
ID ABG19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                       31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY36129-Y36222 represent novel human secreted proteins encoded by extended cDNA sequences represented in AAX97813-X97906. The protein of the invention have cytostatic, thrombotic and osteopathic activity
                     Claim
                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                            Novel human diagnostic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and chromosome mapping expression vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The extended cDNAs can be used to express secreted proteins or them or to obtain antibodies capable of binding to the secreted proteins. They may also be used in diagnostic, forensic, gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                         biodiversity
                                                                                                                               Drmanac
                                                                                                                                                   (HYSE-) HYSEQ
                                                                                                                                                                                                        30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                               food
                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                             ABG19926 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 302; 307pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                              2001-639362/73.
DB; AAS84113.
                                                                                                                                                                                                                                                                                            n; chromosome mapping; supplement; medical ir
                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 MKVDKDRQMVVLEEEFQNISPEELKMELPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \vdash
                                                                                                                               RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNAs encoding secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKVDKDRQMVVLEEEFRNISPEELKMELPERQPRFVVYSYKYVRDDGRVSYPLCFIFSSP
                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                             Liu C,
                                                                                                                                                                       2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                   INC.
                    ID No 50285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duclert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.9%;
98.2%;
                                                                                                                             Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      procedures. Uses also include design of secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,
                                                                                                                                                                                                                                                                                            g; gene mapping; gene therapy; forension
imaging; diagnostic; genetic disorder.
                                                                                                                                ΥT
                   103pp;
                                                                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 558; DB Pred. No. 2.6e 1; Mismatches
                                                                                                                                                                                                                                                                                                                              #19917.
                                                                                                                                                                                                                                                                                                                                                                                              B
                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20;
.6e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               parts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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60

The invention relates to isolated polynucleotide (I) and

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AAG03953
ID AAG03
XX AAG03
AC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed appear in the printed and the printed are intention, but was obtained in the electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG03953 standard; Protein; 116
                                                                                                                                                                                                                                                                                     (GEST ) GENSET
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                                                                                                                                  2000-500381/45.
DB; AAC03959.
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                                                                                                                                                                                                                         Milne Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDROMVVLEEEEFQNISPEELKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----FVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKTRLVQTAELTKV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, SEQ ID NO: 8034.
                                                                                                                                                                                                                                                                                                                                                  99US-0122487
                                                                                                                                                                                                                         J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69.98;
78.58;
                                                                                                                                                                                                                         Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tag; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                         Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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RESULT 13
ABB61879
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Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                     Disclosure;
                                                                                                          New isolated nucleic acid
genes from Drosophila and
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                                                                                                                                                                                                                                                23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                   27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical.
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                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila; developmental biology; cell signalling; insecticide;
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide SEQ ID NO 12429
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                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Best Local S
Matches 69
polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                             Claim 20;
                                                                                                                                                                                                                                                                                              biodiversity
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23-AUG-2000;
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                                                                                                                                                                                        invention
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                                                                                                                                                                                   relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                           ID No 50283; 103pp;
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                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation
                                            Claim 20; SEQ
                                                                                                                                                    WPI; 2001-639362/73.
N-PSDB; AAS84112.
                                                                                                                                                                                               Drmanac RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quantitating a polypeptide in tissue, as molecular weight markers and a a food supplement. (II) and its binding parkers are useful in medical imaging of sites expressing (II), (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polypeptide and polynucleotide sequences have applications.
                                                                          biodiversity
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic of
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                                                                                                                                                                                             Liu C,
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2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                           ID No 50284; 103pp; English
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Pred. No. 4.8e-20;
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Вb
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                                                                                                                                                                                                                                                                                                                                                                              cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome cc and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating cc disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in cc diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and produce other types of data and products dependent on DNA and cd amino acid sequences. ABG00010-ABG30377 represent novel human cd diagnostic amino acid sequences of the invention.

CC diagnostic amino acid sequences of the invention.
Search completed: September 23, 2003, 15:08:48 Job time: 89 secs
                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                    33; Conservative
                                                                                                                                                                                                                                                                                                                                     46 AA;
                                                                                                                                                                                                                                                  22.7%;
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Pred. No. 3.3e-11;
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	ţ	cofilin - chicken	destrin - pig	destrin [validated	DNA-directed DNA p	actin-depolymerizi	hypothetical prote	signal-transducing	hypothetical prote	actin-depolymerizi	cofilin, muscle -	destrin – chicken	recombination prot	hypothetical prote	cofilin - pig

ALIGNMENTS

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A;Molecule type: mRNA
A;Residues: 1-142 <KAP>
A;Cross-references: GB:M86492; GB:M3İ742; NID:g183369; PIDN:AAA58614.1; PID:g183370
C;Comment: This protein promotes the differentiation of normal neurons and glial cell
C;Genetics:
                                                                                                                                                                                                                                                                                                glia maturation factor beta - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999 C;Accession: PT0410 R; Kaplan, R.; Zaheer, A.; Jaye, M.; Lim, R. J. Neurochem. 57, 483-490, 1991 A;Title: Molecular cloning and expression of biologically active human glia maturation A;Reference number: PT0410; MUID:91303115; PMID:1712830 A;Accession: PT0410.
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glia maturation factor-gamma - rat
glia maturation factor-gamma - rat
glia maturation factor-gamma - rat
glia maturation factor-gamma - rat
glia maturation factor-gamma - rat
glia maturation factor-gamma - rat
glia maturation 09-Jun-2000 #text_change 02-Nov-2001
C;Accession: JC7218
R;Tsuiki, H; Asai, K.; Yamamoto, M.; Fujita, K.; Inoue, Y.; Kawai, Y.; Tada, T.; Mor
J. Biochem. 127, 517-523, 2000
A;Fitle: Cloning of a rat glia maturation factor-gamma(rGMFG) cDNA and expression of
A;Reference number: JC7218; MUID:20198266; PMID:10731725
A;Accession: JC7218
A;Accessio
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A;Cross-references: GDB:134671
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Pred. No. 1.6e-56;
7; Mismatches 5;
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C; Superfamily:

glia maturation factor beta

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RESULT 4
$22149
$11a maturation factor beta - rat
G;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
C;Accession: $22149
R;Zaheer, A.
submitted to the EMBL Data Library, December 1991
. Deference number: $22149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lim, R.; Zaheer, A.; Lane, W.S.

RyTitle: Complete amino acid sequence of bovine glia maturation factor across the complete amino acid sequence of bovine glia maturation factor across the complete amino acid sequence of bovine glia maturation factor across the complete amino acid sequence of bovine glia maturation factor beta

C;Keywords: accetylated amino end; growth factor experimental figures.
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GIS maturation factor beta - bovine
GIS maturation factor 
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                                                                                                          A;Cross-references: EMBL:Z11558
C;Superfamily: glia maturation
                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-141 <ZAH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
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  Score 611; DE
Pred. No. 1.5e
l6; Mismatches
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Pred. No. 4e-50;
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Pred. No. 1.4e-50;
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                                                                                                                                   PID: g1334282
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                           DB 1;
.5e-49;
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A; Map position: 1
C; Superfamily: glia maturation factor beta
                                                                                                                                                                                                                    R;Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, August 1997 A;Reference number: 221751 A;Accession: T37977
                                                                                                                                                                                                                                                                                       cofilin/tropomyosin-type actin binding protein - fission C;Species: Schizosaccharomyces pombe C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_C;Accession: T37877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         к; LLU, L.X.; Xu, H.; Weller, P.F.; Shi, A.; Debnath, Gene 186, 1-5, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glia maturation factor - nematode (Brugia malayi)
C;Species: Brugia malayi
                                                                                                                                  A; Experimental source: strain
                                                                                                                                   A;Cross-references: EMBL:Z98597; PIDN:CAB11220.1; GSPDB:GN00066; A;Experimental source: strain 972h-; cosmid c17H9
                                                                                                                                                                    A; Residues: 1-141 <SKE>
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A; Residues: 1-138 <LIU>
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                                                                                                   A; Gene: SPDB:SPAC17H9.11
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              Query Match
Best Local
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les 62; Conserv
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L Similarity
46; Conserv
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                23.8%;
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 29;
Score 175; DB Pred. No. 3.7e
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                                                                                                                                                                                                     GB/EMBL/DDBJ
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                DB 2;
.7e-09;
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MSDSLVVCEVDPELTEKLRKFRFR-KETDNAAIIMKVDKDRQMVVLEEEFQNI-SPEELK 58

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hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein D4245; hypothetical protein D4249; hypothetical C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54047; S58843; S61752; S67879
R;Hunt, S.; Bowman, S.; Harris, D.
submitted to the BMEL Data Library, May 1995
A;Reference number: S54031
A;Accession: S54047
A;Molecule type: DNA
A;Residues: 1-149 <BRA>
A;Residues: 1-149 <BRA>
A;Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
R;Brandt, P.; Ramlow, S.; Otto, B.; Bloecker, H.
Yeast 12, 85-90, 1996
                                                                                                 A;Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAAB9092.1; PID:g798914 R;Brandt, P.; Otto, B.; Ramlow, S.; Blocker, H. submitted to the EMBL Data Library, January 1995 A;Reference number: S58832 A;Accession: S58843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Map position: 3
A:Introns: 9/1; 35/1; 157/3; 200/3; 246/1; 285/3
C:Superfamily: probable tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; CLOSS-references: EMBL:AL034490; PIDN:CAA22475.1; A; Experimental source: strain 972h-; cosmid c126 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
C:Accession: T40910
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A; Residues: 1-149 < HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PNFAFYS - - - LPKDG - - SSKILFIYICPMQATVKHRMVYSSSKLGLLDSIKAELGIVIDG
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Pred. No. 0.00059;
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December 1998
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 RESULT 10
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                                                                                                                                                                                                                                                                                                                            Query Match
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                                                            289
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tyrosine kinase A6 - human (man)
(;Speciles: Homo sapiens (man)
(;Speciles: Homo sapiens (man)
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Dec-2002
C;Accession: A55922
C;Accession: A55922
MOI: Cell. Biol. 14, 982-988, 1994
A;Title: Prokaryotic expression cloning of a novel human tyrosine kinase.
A;Reference number: A55922; MUID:94119116; PMID:7507208
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:U02680; NID:g451481; PIDN:AAC50062.1; C;Superfamily: probable tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: SGD:S0002470
A;Map position: 4R
C;Superfamily: glia maturation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R;Bloecker, H.; Brandt, P.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67587
A;Accession: S67879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-350 <BEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain S288C C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-149 <BLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-149 < BRW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S61752
A; Status: nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z74359; NID:g1431514; PIDN:CAA98881.1; PID:g1431515; MIPS:YD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacch A;Reference number: S61741; MUID:96381250; PMID:8789263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 LIEVSSGLEDDSDVEELREQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 VFEIRT--TDDLTEAWLQEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 LPDNSPRFVLTAYPTTTKDGFKQTPLVLVYWKPMTVVSQEWKMLYAGALEMIREECGTFK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVG-CKPEQQMMYAGSKNRLVQTAELTK 119
                                                                                                                                                                                                                                                                            6 VVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 EVDPELTEKLRKFR-FRKETDN-AAIIMKVD-KDRQMVVLEEEFQNISPE-----ELKME 60
                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                            P----RYVYSYKYYHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE----
                                                                                                                                                                                                                      VAFPISREAFQALEKLNNRQLN---YVQLEIDIKNEIIIL----ANTTNTELK-DLPKRI 229
MDVIRKIEIDNGDELTADFLYEEV
                                                                                                            PKDSARYHFFLYKHSH-EGDYLESIVFIYSMPGYTCSIRERMLYSSCKSRLLEIVERQLQ
                                                         --LTKVFEIRTTDDLTEAWLQEKL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KIGTETRNKIKKFRTSTARTDSIKALSIKIEPKPSYEIIVDEDEQEELDEIEDLSELAEI 65
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                             15.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%;
27.7%;
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                                                                                                                                                                                                                                                                                                                                                             Score 113; DB 2
Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 116.5; DB Pred. No. 0.001;
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  312
                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 350;
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                                                                                                                                                                                                                                                                                                                                      53;
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C; Accession: A86149

R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Luizar, L.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                        Qy
                                                                                        В
                                                                                                                          Qy
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C; Superfamily: co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actin-depolymerizing factor homolog At1g01750 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
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A86149
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C;Superfamily: cofilin
C;Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, April 1998 A;Description: The sequence of A. thaliana F6N23. A;Reference number: 214281 A;Accession: T01232 A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              actin-depolymerizing factor F6N23.12 - Arabidopsis thaliana N;Alternate names: protein F6N23.12 (;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 13-Aug-1999 (;Accession: T01232 R;Geisel, C.
                                                                                                                                                                                                                                                                                                               C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                   A; Residues:
                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                   A; Status:
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A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-133 <GET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 5
                                                                                                                                                                            Matches
                                                                                                                                                                                                                    Query Match
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Best Local
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                                             67
      66
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                                                                                                                                                                                                                                                                                                                                                     1-140 <STO>
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                    RFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTT 126
                                                                                                              RYAVYDYDFTTPENCQKSKIFFIAWSPDTSRVRSKMLYASSKDRFKRELDGIQV-ELQAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVYDFDFTTEDNCQKSKIFFIAWSPDTSRVRSKMLYASSKDRFKREMEGIQV-ELQATD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTID 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEE----LKMELPERQPRF
                                                                                      ELKAK-RNYRF-----IVFKIDEKAQQVMIDKLGNPEETY-----EDFTRSIPEDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKAK-RTYRF-----IVFKIDEKAQQVQIEKLG---NPEETYDDFTSSIPDDECRY 60
                                                                                                                                                                                                                                                                    cofilin
                                                                                                                                                                              Conservative
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                                                                                                                                                                            23; Mismatches
                                                                                                                                                                                                Score 111.5; DB Pred. No. 0.0028;
                                                                                                                                                                                                                                                                                                                               NID:g8671845; PIDN:AAF78408.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 111.5; DB 2; Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                            43;
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                                                                                                                                                                            Indels
                                                                                                                                                                                                                  Length
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  124
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T46362
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <AAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable tyrosine kinase DKFZp43400516.1 [similarity] - human C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_chance;Accession: T46362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z14110; NID:g22747; PIDN:CAA78483.1; PID:g22748 C;Superfamily: cofilin C;Keywords: actin binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        actin-depolymerizing factor - trumpet lily
C;Species: Lilium longiflorum (trumpet lily)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
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R;Kim, S.R.; Kim, Y.; An, G.
Plant Mol. Biol. 21, 39-45, 1993
A;Title: Molecular cloning and characterization of anther-preferential cDNA encoding A;Reference number: $30934; MUID:93144690; PMID:8425049
A;Accession: $30935
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S30935
                                                                                                                                                                                                                                                                                                                               C; Superfamily: probable tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                     A; Note: DKFZp43400516.1
                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: adult
                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AL136773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T46362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the Protein Sequence Database, January
A; Reference number: 223037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Koehrer, K.;
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A; Residues: 1-139 <KIM>
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Matches 37
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                                                                                                                                                                                                                                                               Local Similarity
                        119
                                                                                                                                                     182
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                                                                                                                                                                                           10 VDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53
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37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YDDFTECLPPNECRYAVFDFDFVTDENCQKSKIFFISWSPDTSRVRSKMLYASTKDRFKR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D 127
                    KVFEIRTTDDLTEAWLQEKL 138
                                                             ARYHFFLYKHTH-EGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIA 292
                                                                                                        -RFVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTA-----ELT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MSDSLYVCEVDPELTEKL-----RKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQ-NIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D 125
                                                                                                                                                     LQPEAQRALQQL---KQKMVNYIQMKLDLERETI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELDGIQV-ELQATD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEELKMELPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MANSSSGMAVDDECKLKFMELKAKRNFRF-----IVFKIEEKVQQVTVERLGQPNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beyer, A.; Mewes, H.W.; Gassenhuber,
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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26.4%;
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                                                                                                                                                                                                                                                               Score 109; DB 2
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 109; DB 2; Pred. No. 0.0048;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              DKFZp43400516
                                                                                                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                           51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.; Wiemann,
2000
                                                                                                                                                     -ELVHTEPTDV-AQLPSRVPRDA
                                                                                                                                                                                                                                                                                    Length 349;
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                                                                                                                                                                                                                                         Indels
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probable tyrosine kinase F38E9.5 [similarity] - Caenorhabditis elegans C. Species: Caenorhabditis elegans C. Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002 C. Accession: T30015 R.Wu, X.; Gattung, S.
                                            δÃ
                                                                                                                                                                                                                                                                                  A;Map position: 3
A;Introns: 43/1; 84/2
A;Note: F16L2.200
C;Superfamily: cofilin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  actin depolymerising like protein - Arabidopsis thaliana N;Alternate names: protein F16L2.200 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000 C;Accession: T47539
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                                                                                               д
                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-133 <JOR>
A;Cross-references: EMBL:AL162459
A;Experimental source: cultivar Columbia; BAC clone F16L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
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A;Introns: 9/1; 83/2; 123/3; 169/3; 197/3; 248/1; 288/3; 312/3
C;Superfamily: probable tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-357 <WUX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wu, X.; Gattung, S. submitted to the EMBL Data Library, January 1996 A;Description: The sequence of C. elegans cosmid F38E9. A;Reference number: Z20722
                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z24468
A; Accession: T47539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, March 2000
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 -----LTKVFEIR------TTDDLTEAWLQE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 PRYTFYNFDHTW-EGVPQQCTLFIYSLPSSGSSIKERMLYSSCKGPFLSAAQNQYGVVIT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 NKFLQKRSNKMFKIREKIFLKRLKNDMEVDARDDLSEKALLE 328
       64
                        67 RFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTT 126
                                                                                          13 ELKER-RTFR-----SIVYKIEDNMQVIVEKHHYKKMHGEREQSYEEFANSLPADEC 63
                                                                                                                                 13 ELTEKLRKERFRKETDNAAIIMKVDKDRQMVVLEEEFQNI-----SPEELKMELPERQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 PREVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 37; Conserv
                                                                                                                                                                                                                  Similarity
RYAILDIEFVPGERKI----CFIAWSPSTAKMRKKMIYSSTKDRFKRELDGIQV-EFHAT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKIEIGDGAELTAEFLYDEV 312
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                                                                                                                                                                                     14.1%; Score 103.5; DB 26.4%; Pred. No. 0.015; ative 30; Mismatches
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Search completed: September 23, 2003, 15:11:51 Job time: 42 secs

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ACTF_ACACA
ADF2_ARATH
ADF6_ARATH
ADF6_ARATH
ADF6_ARATH
ADF_BRANA
TWF1_YEAST
ADF3_MAIZE
ADF5_ARATH
COF1_HUMAN
COF1_RAT
COF1_PIG
RMUC_CHLTR
RECN_AQUAE
COF2_WENLA
DEST_CHICK
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                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  EMBL; AB001993; BAA25572.1; EMBL; AF038956; AAC39870.1;
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	sapiens (Human).
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
	D=9606;
	[1] SEQUENCE FROM N.A.
	INE=98207713; PubMed=9545571;
	L'Ca >.,
	MORIYAMA A., KATO Y.; "Isolation of novel human cDNA (hGMF-qamma) homologous to Glia
	•
	Biochim. Biophys. Acta 1396;242-244(1998). [2]
	SEQUENCE FROM N.A.
	WEDITNE=Blood;
	J.
	J., Yu YP., Xu SH.,
	CD34(+)
	Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
	[3] SEOUENCE FROM N.A.
	MEDLINE=20009844; PubMed=10541589;
	D.N., Jenkins R.B.;
	"The human glia maturation factor-gamma gene: genomic structure and
	ssor ber
	-!- TISSUE SPECIFICITY: EXPRÉSSED PREDOMINANTLY IN LUNG, HEART, AND
	PLACENTA!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
	This SWISS-PROT entry is copyright. It is produced through a collaboration hetween the Swiss Institute of Bidinformatics and the EMMI outstation -
	between the awas institute of broinformatics and the Emph Outstation of its the European Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way.

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Matches 142
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
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GO; GO:0008047; F:enzyme activator activity; TAS.
GO; GO:0004860; F:protein kinase inhibitor activity; GO; GO:0004860; P:protein amino acid phosphorylation; InterPro; IPR002108; Actbind_cofin.
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SMART; SM00102; ADF; I.
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16-OCT-2001 (Rel. 40, I
Glia maturation factor
                   SPECIES=Human;
MEDLINE=95321959;
                                                             PHOSPHORYLATION.
                                                                                                  Lim R., Zaheer A., Lane W.S.; "Complete amino acid sequence Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                          SPECIES-Bovine;
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J. Neurochem. 57:483-490(1991).
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AF108023; AAD27807.1;
AF108024; AAD27807.1;
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PIR; PT0410;
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GO:0004860; F:protein kinase inhibitor activity; TAS.
GO:0004871; F:signal transducer activity; TAS.
GO:0007399; P:neurogenesis; TAS.
GO:0007365; P:protein amino acid phosphorylation; TAS.
GO:0007165; P:signal transduction; TAS.
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SEÓUBNACE FROM N.A.
MEDLINE-93171924; PubMed-8436977;
Zaheer A., Fink B.D., Lim R.;
"Expression of glia maturation factor

beta mRNA and

protein

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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat

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Rattus norvegicus (Rat).

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Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
                                                                                                                                                                                                                                                                                                                                                                                                  ADFX_ARATH STANDARD; PRT; 140 AA.

Q9LQ81;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
ACTIO-depolymerizing factor like At1g01750 (ADF-like).
AT1G01750 OR TIN6.16.
                                                                                                                                                                                                                          STRAIN=cv. Columbia;
MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00241; cofilin_ADF; SMART; SM00102; ADF; 1. Growth factor; Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organs and cells.";
J. Neurochem. 60:914-920(1993).
-!- FUNCTION: THIS PROTEIN CAUSES DIFFERENTIATION OF BRAIN CELLS,
STIMULATION OF NEURAL REGENERATION, AND INHIBITION OF
PROLIFERATION OF TUMOR CELLS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
SUBFAMILY.
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
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80.7%;
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No. 6.1e-49;
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ARESULT 5
ADF_L
ADF_L
AC P3017
AC 01-Ap
DT 01-Ap
DT 28-FE
Actin
OS L1114
OC EUKAR
OC L114
OC L114
OC L116
OX NCB1_
RN (10)
RP SEQUE
RC STRAI
RX MEDLI
RA Kim SCOL
RA Kim SCOL
CC -i-F
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CC -i-F
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Best Local S
Matches 34
Kim S.-R., Kim Y., An G.;
"Molecular cloning and characterization of anther-preferential cDN encoding a putative actin-depolymerizing factor.";
plant Mol. Biol. 21:39-45(1993).
-i- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
-i- TISSUE SPECIFICITY: PREFERENTIALLY IN MATURE ANYHER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF_LILLO
P30175;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=cv. Nellie white; TISSUE=Pollen;
MEDLINE=9314469; PubMed=8425049;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Actin-depolymerizing factor (ADF).
Lilium longiflorum (Trumpet lily).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as Its content is in the modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD002129; Actbind_cofln; 1.
SMART; SM00102; ADF; 1.
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Pfam; PF00241; cofilin_ADF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4690;
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HSSP; Q39250; 1F7S.
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                                                                                                                                                              of anther-preferential cDNA
y factor.";
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ADF1_ARATH

ADF1_ARATH

ADF1_ARATH

ADF1_ARATH

AC Q39250;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Actin-depolymerizing factor 1 (ADF-1) (AtADF1).

GN ADF1 OR AT3446010 OR F16L2_220.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Purosids II; Brassicales; Brassicaceae; Arabidopsis.
     RESULT 6
ADF1_A
ADF1_ATH
ID ADF1_A
AC Q39250
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
DT 28-FEB
OC SPETIAL
OC SPETIAL
OC SPETIAL
OC SPETIAL
OC STRAIN
RC STAGE
RT POLYME
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                          Staiger C.J., Ashworth S.L.;
"Actin depolymerizing factor from Arabidopsis thaliana severs polymers and binds to monomers in a pH-dependent manner.";
                                              STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PDUUZIZ;
SMART; SM00102; ADF;
BROSITE; PS00325; AC
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       Salanoubat M., Lemo Fartmann B., Valle
                                                                                SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
                                                                                                                                                           Plant Mol.
                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
MEDLINE=21307188; PubMed=11414611;
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., STRAIN-cv. Columbia
                                                                                                                                                                                                                                                                                                                                                                Submitted
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PIR; S30935; S30935.
HSSP; Q39250; 1F7S.
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Pfam; PF00241; cofilin_ADF; 1.
                                                                                                                                                 g C.-H., Kost B., Xia G., Chua N.-H.; lecular identification and characterization DF1, AtADF5 and AtADF6 genes."; nt Mol. Biol. 45:517.527(2001).
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                            Lemcke K., Rieger
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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     Perez-Alonso
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Unseld M., M., Obermai
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       Obermaier
                                                                                                                                                                                                       Arabidopsis
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RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Myakatura G.,
RA Wezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Myakatura G.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Roore P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Muraki A.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT Tablata S.;
RT Tablata S., Nakaraki N., Shinpo S., Tabata S.;
RT Tablata S., Nakaraki N., Shinpo S., Tabata S.;
RT Tablata S., Sanco S., School S., Kato T., Asamizu E.,
RA Watanabe A., Yasuda M., Tabata S.;
RT Tablata S.;
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00325; ACTIN DEPOLYMERIZING; 1.
Actin-binding; Multigene family; 3D-structure.
Actin-binding; Multigene family; 3D-structure.
DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
SEQUENCE 139 AA; 16112 MW; E9429E0FE23A944F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; 1F7S; 15-NOV-00.
InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U48938; AAB03696.1; -. EMBL; AF102173; AAC72407.1; EMBL; AL162459; CAB88325.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00102; ADF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (F-ACTIN) AND BINDS TO ACTIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: ACTIN DEPOLYMERIZING PROTEIN.
(F-ACTIN) AND BINDS TO ACTIN MONOMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A comparative structural analysis of the ADF/cofilin family."; Proteins 41:374-384(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20481864; PubMed=11025548;
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                                                                                                                                                                                                                                                                                                               Local
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75
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                                       VHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD
VTAENCQKSKIFFIAWCPDIAKVRSKMIYASSKDRFKRELDGIQV-ELQATD
                                                                                                                                       KLRFLELKAKRTHRFIVYKIEEKQKQVVVEKVGQPIQTYEEFAACLPADECRYAIYDFDF
                                                                                                                                                                                                    KLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISP-EELKMELPERQPRFVVYSYKY
                                                                                                                                                                                                                                                                               Conservative
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27.78;
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                                                                                                                                                                                                                                                                                                            Score 108; 1
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RESULT

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RESULT 8
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Matches 28
  ADF3_ARATH
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EMBL; AB015475; BAB08357.1;
HSSP; Q39250; 1F7S
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Dong C.-H., Kost B., Xia G., Chua N.-H.;
"Molecular identification and characterization
AtADF1, AtADF5 and AtADF6 genes.";
Plant Mol. Biol. 45:517-527(2001).
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _ARATH
ADF4_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002129; Actbind_cofin; 1.
SMART; SM00102; ADF; 1.
PROSITE; PS00325; ACTIN_DEPOLYMERIZING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structural analysis of Arabidopsis thaliana chromosome 5. Sequence features of the regions of 1,013,767 bp covered by physically assigned P1 and TAC clones.";
DNA Res. 5:297-308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00241; cofilin_ADF;
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Nakamura Y., Sato S., Asamizu E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002108; Actbind_cofln.
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                                                                                                                       VTAENCQKSKIFFIAWCPDVAKVRSKMIYASSKDRFKRELDGIQV-ELQATD
                                                                                                                                                                  VHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD
                                                                                                                                                                                                                                            KLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNI-SPEELKMELPERQPRFVVYSYKY
                                                                                                                                                                                                                     KLRFLELKAKRTHRFIVYKIEEKQKQVIVEKVGEPILTYEDFAASLPADECRYAIYDFDF
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                                                                                                                                                                                                                                                                                                                                                                                                                    139 AA;
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117
134
                                                                                                                                                                                                                                                                                                                        Conservative
  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                      16034 MW;
                                                                                                                                                                                                                                                                                                                                             14.3%;
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                                                                                                                                                                                                                                                                                                                                             Score 105; DB 1; Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING (POTENTIAL).
I -> R (IN REF. 1).
L -> W (IN REF. 1).
PRT;
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                                                                                                                                                                                                                                                                                                                        Mismatches
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139
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-cv. Columbia;
STRAIN-cv. Columbia;
MEDLING-21307188; PubMed-11414611;
MODIG C.-H., Kost B., Xia G., Chua N.-H.;
"Molecular identification and characterization ataDF1, AtaDF5 and AtaDF6 genes.";
Plant Mol. Biol. 45:517-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF102821; AAD09109.1; -. EMBL; AB015475; BAB08356.1; -. EMBL; AF3061059; AA25879.1; -. HSSP; Q39250; 1F7S.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00325; ACTIN_DEPOLYMACTIN-binding; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00102; ADF; 1.
PROSITE; PS00325; ACTIN_DEPOLYMERIZING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.lsb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     physically assigned P1 and DNA Res. 5:297-308(1998).
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MEDLINE=99087489;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002108; Actbind_cofln.
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                                                                                                                                                                                                                                     . Similarity
27; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD002129; Actbind_cofin; 1.
VHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD 127
                                                                                                                                                                  KLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQ-NISPEELKMELPERQPRFVVYSYKY
                                                                                                  KLKFMELKTKRTHRF I I YK I EELQKQV I VEK I GEPGQTHEDLAASLPADECRYA I F DF DF
                                                                                                                                                                                                                                                                                                                                                                        139 AA;
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S., Asamizu E.,
                                                                                                                                                                                                                                                                                                                                                                            15922 MW;
                                                                                                                                                                                                                                                                     14.18; 24.18;
                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                     Score 104; 1
                                                                                                                                                                                                                              Pred. No. 0.00
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            D3325AA71D0D102E CRC64;
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                                                                                                                                                                                                                       J.0081;
50;
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                                                                                                                                                                                                                                                                                                     Length 139;
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RESULT 9

ADF1_PE ADF1_P

ADF1_P AC Q9FVI2

DT 28-FEB

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DR INTERF

DR INTERF

DR SMART;

DR SEQUEN
  RESULT 10
ADF2_PETHY
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Best Local S
Matches 29
                                                                                                                                                                    20-FEB-2003 (Rel. 41, C
28-FEB-2003 (Rel. 41, L
28-FEB-2003 (Rel. 41, L
Actin-depolymerizing fa
ADF2.
                                                                                                                                                                                                                                   ADF2_PETHY
Q9FVI1;
28-FEB-2003
28-FEB-2003
28-FEB-2003
Spermatophyta; Magnoliophyta; eudicotyledons; core eu Asteridae; lamiids; Solanales; Solanaceae; Petunia. NCBI_TaxID=4102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  PETHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR002108; Actbind_cofln
Pfam; PF00241; cofilin_ADF; 1.
ProDom; PD002129; Actbind_cofln; 1
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Mun J.-H., Yu H.-J., Lee H.S., Kwon Y.M., Lee J.S., Lee I
"Two closely related cDNAs encoding actin-depolymerizing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Actin-depolymerizing factor 1 (ADF 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00325; ACTIN_DEPOLYMI
Actin-binding; Multigene family
DOMAIN 92 111 AC
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Spermatophyta; Magnoliophyta; eudicotyledor
Asteridae; lamiids; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Petunia hybrida (Petunia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENT (F-ACTIN) AND BINDS TO ACTIN MONOMERS (By similarity). SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity
29; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLRFLELKAKRTHRFIVYKIEEKQKQVVVEKIGEPTESYEDFAASLPENECRYAVYDFDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIN_DEPOLYMERIZING;
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                                                                                                                                                                                                     , Last sequence update)
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factor 2 (ADF 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 103; DB Pred. No. 0.01
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                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             008073E2CAA28F0B CRC64;
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                                                                                                                                                                                                                                                                                                                                                     143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 139;
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                                                                                         eudicots;
                                                                                                              Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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RESULT 11
ACTP_ACACA
   A CONTRACTOR OF THE PROPERTY O
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for concentitles requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                   This
                                Blanchoin L.,
                                   MEDLINE=98411306; PubMed=9737968;
Blanchoin L., Pollard T.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93363583; PubMed=8357799; Quirk S., Maciver S.K., Ampe C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acanthamoeba castellanii (Amoeba)
Eukaryota; Acanthamoebidae; Acant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1994
01-OCT-1994
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pfam; pr00241; cofilin_ADF; 1.
priNTS; pr000006; COFILN.
proDom; pD002129; Actbind_cofln; 1.
                                                                                                    X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
                                                                                                                                                                                                            Acanthamoeba.
                                                                                                                                                                                                                                        "Crystal structure of the
                                                                                                                                                                                                                                                                            MEDLINE=97290450; PubMed=9145107; Leonard S.A., Gittis A.G., Petrella E.C.
                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actophorin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF183904; AAG16974.1; HSSP; Q39250; 1F7S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENT (F-ACTIN) AND BINDS TO ACTIN MONOMERS (By similarity).
-i- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20534787; PubMed=11080583; Mun J.-H., Yu H.-J., Lee H.S., Kwo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
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E; PS00325; ACTIN_DEPOLYMERIZING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD
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                                Pollard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 100.5; DB Pred. No. 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTIN-BINDING (POTENTIAL).
408E0353DE61C05C CRC64;
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Acanthamoeba actophorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEVERS ACTIN FILAMENTS
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                                                                                                                                                                                                                                                actophorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaiser
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INIT_MET 0
MOD_RES 1
DOMAIN 86
ADF2_ARATH STANDARD; PRT; 137 AA. 039251; O9LZT2; 28-FEB-2003 (Rel. 41, Created) / 28-FEB-2003 (Rel. 41, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) 28-FEB-2003 (Rel. 41, Last annotation update) Actin-depolymerizing factor 2 (ADF-2) (AtADF2). ADF2 OR AT3G46000 OR F16L2_210.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ADF/cofilin) and profilin.";
J. Biol. Chem. 273:25106-25111(1998).
-i- FUNCTION: FORMS A ONE TO ONE COMPLEX WITH MONOMERIC ACTIN. CI-REGULATE THE POOL AVAILABLE FOR POLYMERIZATION. SEVERS ACTIN FILAMENTS IN A DOSE-DEPENDENT MANNER.
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                     TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00006; COFILIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00241; cofilin_ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Monomer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1CNU; 01-JUN-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M93361; AAA02909.1;
                                                                                                                   84 WAPDSAPIKSKMMYTSTKDSIKKKLYGIQV-EVQATDAAEISEDAVSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; PD002129;
SM00102; AI
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00325; ACTIN_DEPOLYMERIZING;
                                                                                                                                      SSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTD--DLTEAWLQEK 137
                                                                                                                                                           VTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDCRYAIFDYEFQVDGGQRN-KITFIL
                                                                                                                                                                              IIMKVDKDRQMVVLEE-EFQNISPEELKMELPERQPRFVVYSYKYVHDDGRVSYPLCFIF
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                                                                                                                                                                                                      Conservative
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25.7%;
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                                                                                                                                                                                                              Score 97.5;
Pred. No. 0
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                                                                                                                                                                                                            .031;
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RA Fartmann B., Valle G., Bloecker H., Perez-Alconso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Pulgdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Winckelmann R., Kranz H., Voss H., Holland R., Benes V.,
RA Winckelmann R., Kranz H., Voss H., Holland R., Benes V.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Benes T.,
RA Wiedelmann R., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H., Tallon L.J., Sheat T.P.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H., Tallon L.J., Sheat T.P.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H., Tallon L.J., Sheat T.P.,
RA Prauss D., Lin X., Nierman M.C., Salzberg S., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Muraki A.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT Thilana T.,
Kaneko T., Makamura Y., Sato S., Watana A.,
Watanabe A., Yamada M., Yasuda M., Tabata S.;
Thaliana T.,
Kaneko T., Makamura Y., Sato S., Watana A.,
Kaneko T., Nakamura Y., Sato S
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                           ProDom; PD002129; Actbind_cofln; 1.
SMART; SM00102; ADF; 1.
PROSITE; PS00325; ACTIN_DEPOLYMERIZING;
                                                                                                                                                                                                                  EMBL; U48939; AAB03697.1; ...
EMBL; AL162459; CAB82824.1; ALT_INI
EMBL; AL162459; CAB82824.1; ALT_INI
HSSP; Q39250; IF7S.
InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Actin depolymerizing factor from Arabidopsis thaliana severs polymers and binds to monomers in a pH-dependent manner."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence and analysis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salanoubat M., Lemcke K., Rieger M.,
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                                                                                                                       Actin-binding; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21016720; PubMed=11130713;
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long
                                                                      137 AA;
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                                                                         15745 MW;
12.9%;
25.2%;
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Score 95;
Pred. No.
                                                                                                  ACTIN-BINDING
                                                                         BE28852817394046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ansorge W., Unseld M.,
                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                           DB 1;
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                      Length 137;
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RESULT ADDROLL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Actin-depolymerizing factor 6 (ADF-6) (AtADF6).
ALDF6 OR ATZG31200 OR F16D14.4.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core
eurosids II; Brassicales; Brassicaceae; Arabidopsi
                                                                                     EMBL;
                                                                                                                                                  EMBL;
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Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced
SSP consortium (Salk/Stanford/PGEC).";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D. Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Chernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          modified
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"Molecular identification and characterization
AtADF1, AtADF5 and AtADF6 genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21307188; PubMed=11414611;
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Lhaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plant Mol. Biol. 45:517-527(2001).
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                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENT (F-ACTIN) AND BINDS TO ACTIN MONOMERS. PTM: Phosphorylated. SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                      AF102824; AAD09112.1; -
AF18576; AAF01035.1; -
AC006593; AAD20665.2; -
AC057719; AAL15349.1; -
AF372880; AAK49596.1; A
039250; 1F75.
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edons; core eudicots; Rosidae;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Skelton J., Simmonds M., Squares D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti E., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880(2002).
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Best Local
Kawamukai M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION &
PREPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COFI_SCHPO
P78929;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schizosaccharomyces pombe (fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; pF00241; cofilin_ADF; 1.
prINTS; pR00006; COFILIN.
proDom; pD002129; Actbind_cofin; 1.
SMART; SM00102; ADF; 1.
prOSITE; pS00325; ACTIN_DEPOLYMERIZING; FALSE_NEG.
                                                                                                                                     SEQUENCE
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
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GeneDB_SPombe; SPAC20G4.06c; -.
InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofflin_ADF; 1.
PRINTS; PR00006; COFILIN.
ProDom; PD002129; Actbind_cofln; 1.
SMART; SM00102; ADF; 1.
                                                                        OOFI_DICDI STANDARD; PRT; 137 AA
P54706;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D89939; BAA14039.1; -. EMBL; Z98600; CAB11258.1; -. EMBL; T43245.
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                                                                                                                                                                                                                       (COFA OR COF1) AND (COFB OR COF2). Dictyostelium discoideum (Slime mc Eukaryota; Mycetozoa; Dictyostelii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN 88 SEQUENCE 137 AA;
                                                                                                                                                                                                                                                                     Cofilin.
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=44689;
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                                    FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY BIND G- AND F-ACTIN IN A 1:1 RATIO OF COPILIN TO ACTIN. IT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY
SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC
                MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC (BY SIMILARITY).
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Best Local
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Dictypb; DD01059; cofB.
InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
PRINTS; PR00006; COFILIN.
ProDom; PD002129; Actbind_cofln; 1.
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-i- MISCELLANDOUS: THERE ARE TWO GENES FOR COFILIN IN D.DISCOIDEUI
THEY ENCODE FOR IDENTICAL PROTEINS.
-i- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
                                                                                                                                                                                                                                                                               PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
Nuclear protein; Actin-binding; Cytoskeleton; Multigene family.
SEQUENCE 137 AA; 15224 MW; 0C0B0673354F46F3 CRC64;
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                                                                                                                                                Query Match
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Asai K., Kawai Y., Inoue Y., Ueki T., Yamamoto M., Miura Y., Kato T.;
"Homo sapiens Glia Maturation Factor gamma (GMFG) genomic DNA.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040440; BAB86591.1; -.
InterPro; IPR002108; Actbind cofin.
Pfam; PF00241; cofilin_ADF; 1.
SMART; SM00102; ADF; 1.
SMART; SM00102; ADF; 1.
                                                                                                                                                                                                                                                                                                                         Q8TDZ6 PRELIMINARY; PRT; 142 AA. Q8TDZ6; Q1TDZ6; Q1-JUN-2002 (TrEMBLrel. 21, Created) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update) Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update) Q1-QCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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G	4	ω	N	1	0	9	œ	7	σ	G	4	ω	N	_	0	9	æ	7	9	Ŋ	4	ω	N	_	0	9	8	7
91.5	92.5	92.5	93.5	95	95.5	96	97.5	98.5	98.5	99	100.5	102.5	102.5	102.5	103.5	104	104.5	105	106	107	109	109.5	110	110	111	111	111.5	111.5
12.4	12.6	12.6	12.7	٠	13.0	13.1	13.3	13.4	13.4	13.5	13.7	•	13.9	13.9	14.1	14.1	14.2	14.3	14.4	14.6	14.8	14.9	15.0				15.2	
137	137	130	137	146	130	139	142	350	350	153	130	145	140	138	133	145	156	132	129	138	349	343	347	143	• 349	347	140	133
10	10	10	10	10	10	10	10	11	11	10	10	10	10	υī	10	10	σ	10	10	10	4	υ	1	10	11	=	10	10
Q8H2B6	Q8LFH6	Q9FHC4	Q8н2в7	Q8LCM6	049606	Q8H2P8	Q43655	009132	Q91YR1	Q9FWC0	065603	Q9AY76	Q9M594	Q8T1J2	Q9LZT3	Q8H9D5	Q8MIK3	Q94A13	Q9SW69	Q9XEN2	Q9Y3F5	Q9VFM9	Q9DCK8	Q8SAG3	Q9Z0P5	Q8BN77	Q8LCH3	065277
Q8h2b6 nicotiana t	•	Q9fhc4 arabidopsis		Q81cm6 arabidopsis		Q8h2p8 oryza sativ	Q43655 triticum ae	009132 mus musculu			O65603 arabidopsis		Q9m594 elaeis guin	\mathbf{p}		Q8h9d5 solanum tub	σ		Q9sw69 malus domes	١٠		Q9vfm9 drosophila	Q9dck8 mus musculu	Q8sag3 vitis vinif	mus		ch3	065277 arabidopsis

ALIGNMENTS

Оy			
	Qy Db	Qу	Best Loc Matches
121 FEIRTTODLTEAWLQEKLSFFR 142 	61 LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120 	1 MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDROMVVLEEEFONISPEELKME 60 	Hest Local Similarity 98,88; Freq. No. 9.5e-53; Matches 140; Conservative 1; Mismatches 1; Indels 0; Gaps

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Susuki H., Sato K., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Munshaw-Horis A., Yoshida K., Hasegaya Y. Kawati H., Kohtsuki S.
                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-2001) to the EMBI EMBL; ARC97221; AAG22804 1; --
EMBL; AK014214; BAB29210.1; --
EMBL; AK002834; BAB22932.1; --
EMBL; AK009967; BAB26617.1; --
EMBL; BC011488; AAH11488.1; --
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Glia maturation factor-gamma (0610039G16Rik protein) (2310057N07Rik
protein) (Glia maturation factor, gamma).
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                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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Hayashizaki Y.;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection.";
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LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
                                                                                                                  MSDSLVVCEVDPELKETLRKFRFRKETNNAAIIMKVDKDRQMVVLEDELQNISPEELKLE
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                                                                                                                                                                                                                                                                                                                                                                 142
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93.78;
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Pred. No. 4.1e-60;
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                                                                                                                                                                                                                                        Mismatches
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RESULT 4
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Best Local 9
                                                                                                   Bourgeois F., Guimiot F., Mas C., Bulfon Moalic J.M., Simonneau M.;
"Identification and isolation of a full-
(Gmfb), a putative intracellular kinase expressed in telencephalon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-2001) to the EMBL/Ge
EMBL; BC005359; AAH05359.1; -.
InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 1.
SMART; SM00102; ADF; 1.
SEQUENCE 154 AA; 18110 MW; 712E
                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                            Cytogenet. Cell Genet. 92:3
EMBL; AF297220; AAG22803.1;
                                                                                                                                                                                                                    STRAIN=Swiss/IOPS MEDLINE=21328893;
                                                                                                                                                                                                                                                                                                                                                                                                                         Glia maturation
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                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                    GMFB.
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                  InterPro;
                                         MGD; MGI:1927133;
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                    IPR002108; Actbind_cofln
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                                                                                                                                                                                                                                                                                                                                                                                                                         factor-beta
                                           Gmtb
                                                                                                                                                                                                                    OF1; TISSUE=Telencephalon PubMed=11435704;
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82.3%;
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16,
21,
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17, L
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Last annotation update)
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Sciurognathi; Muridae
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                                                                                                                                                                                             Bulfone A.,
                                                                                                                          full-length clone of mouse GMFB inase regulator, differentially
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., Ge Bonaldo M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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Best Local S
   Submitted (NOV-2002) to the EMBL; AK013970; BAB29092.1; EMBL; AK013947; BAB29076.1; EMBL; AB050013; BAB41099.1; EMBL; BC040233; AAH40233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki v.;
"Functional annotation of a
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
3110001016Rik protein (3110001H22Rik protein) (Glia
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GMFB OR 3110001016RIK OR 3110001H22RIK OR
                                                                                                                                                                             TISSUE=Eye;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                            Utsuyama M., Shiraishi J., Hirokawa K.;
"GLIA MATURATION FACTOR PRODUCED IN THYMIC EPITHELIAL CELLS PLAYS
ROLE IN T CELL DIFFERENTIATION IN THE THYMIC MICROENVIRONMENT.";
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Utsuyama M., Shiraishi J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9CQI3
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16722
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                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          full-length mouse cDNA collection.";
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Pred. No. 1.1e-52;
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Sciurognathi;
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Q9VJL6 PRELIMINARY; PRT; 138
Q9VJL6; Q9NK59;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequenc
01-MAR-2003 (TrEMBLrel. 23, Last annotat
01-MAR-003 (TrEMBLrel. 23, Dast annotat
CG5869 protein (BG.DS02740.9 protein).
BG:DS02740.9 OR BCDNA:SD03793 OR CG5869.
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SQ DR DR
                                                                                                                                                                                            Query Match
Best Local Sim
Matches 111;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9IBG6 PRELIMINARY; PR
Q9IBG6; O1-OCT-2000 (TrEMBLrel. 15, Crea
01-OCT-2000 (TrEMBLrel. 20, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Glia maturation factor beta.
Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Cr
Actinopterygii; Neopterygii; Tel
Cyprindae; Cyprinus.
                                                                                                                                                                                                                                                           Fujiki K., Nakao M., Shin D., Yano T.;

"Molecular cloning of a carp homolog of glia maturation submitted (MAY-199) to the EMBL/GenBank/DDBJ databases.

EMBL; AB02699; BAA95482.1; -.

Interpro; IPR002108; Actbind_cofin.

Pfam; PF00241; cofilin_ADF; I.

SMART; SM00102; ADF; 1.

SMART; SM00102; ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1927133; Gmfb.
InterPro; IPR002108; Actbing
Pfam; PF00241; coffiln_ADF;
SMART; SM00102; ADF; 1.
SEQUENCE 142 AA; 16723 M
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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FEIRTTDDLTEAWLQEKLSFFR 142
||:| |||| ||:|||||||
FEVRNPDDLTEEWLKEKLSFFR 142
                                                                                  LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                                                                                               MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
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                                                                                                                                MSSSLVVCEVDGSLQEKLKKFRFRKETSNAAILMKIDMEKQLVVLEEEEYENISLDELREE
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                                                                LPERQPRYIVYSYKLTHGDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQSADLTKI
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78.2%;
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in_ADF; 1.
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                                                                                                                                                                                            Score 600; DB
Pred. No. 7.5e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last annotation
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سم. 1.
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Ostariophysi; Cypriniform
                                                                                                                                                                                                           DB 13;
.5e-51;
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.6e-52;
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Last sequence update)
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138

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RA Adams AD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams AD., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams AD., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Pfeiffer B.D.,
RA Burtis C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendala J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Burtis K.C., Busan D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerbios B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA Gebabios B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M.,
RA Goldek C., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Diegwam C.,
RA Hashi M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Melson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stropski M.P., Smith T.,
RA Spier E., Sandan D.A., Weinstock G.M., Weissenbach J.,
RA J., Sheng L.,
RA J., Sheng L., Sheng L.,
RA J., Sheng L., Sheng L.,
RA J., Sheng L., She
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Evans C.A.,
                                                                                                                                                                                                                                Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Goralez M., Hock J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome., submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N. Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Sahburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R., Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Carlson J.W., Center A., Champe M., Davenport L.B., D
                                                                                                                                                                                            SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kronmiller B., Wan K.H., Holt K.A.,
Amanatides P.G., Brandon R.C., Rogers Y.,
Beson K.Y., Busam D.A.,
Ranzon J., Beeson K.Y., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hexapoda; Insecta; Pterygota;
                                                                                                                                                              Campbell K.
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RESULT 8
Q17247
ID 0172
AC 0172
AC 0172
DT 01-N
DT 01-M
DT 01-M
DT 01-M
DE 611a
GN BNGM
OS Brugg
OC Euka
ON NCBII
RN [1]
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Best Local S
Matches 72
Eukaryota; Metazo
Onchocercidae; Br
NCBI_TaxID=6279;
[1]
                                                                                                01-NOV-1996
01-NOV-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A., Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R., Zieran L.L., Rubin G.M.;

Zieran L.L., Rubin G.M.;

Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003650; AAF53517.2; -...

EMBL; AE003415; AAF44499.1; -...

EMBL; AE003415; AAF44499.1; -...

ENBBL; AE003415; AAF4499.1; -...

Toterpro; IPR002108; AGCDINICOSTIN.

FinyBase; FBgn002894; BG:DS02740.9.

Interpro; IPR002108; Actbind_cofin.

Ffam; PF00241; cofilin_ACDF; 1.
                                                                                                                                             Q17247
Q17247;
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                                                       Brugia malayi.
                                                                        BMGMF
                                                                                    Glia maturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doy
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation of Drosophila melanogaster genome.
                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                               121
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                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                   FEIRTTDDLTEAWLQEKL
                                                                                                                                                                                                                                                                                                                                                 MSDN-QICDISNEVLEELKKFRFSKSKNNAALILKVDREKQTVVLDEFIDDISVDELQDT
                                                                                                                                                                                                                                                                                                                                                                              MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
                                                                                                                                                                                                                                  YEIRELDELTEEWLKAKL
                                                                                                                                                                                                                                                                                        LPGHQPRYVIYTYKMVHDDQRISYPMCFIFYTPRDSQIELQMMYACTKSALQREVDLTRV 119
                                                                                                                                                                                                                                                                                                       LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM
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                                           Metazoa;
                                                                                                                (TrEMBLrel.
                                                                                    (TrEMBLrel.
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                                                                                                                                                            PRELIMINARY;
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                              Brugia
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                                                                                                                                                                                                                                                                                                                                                                                                                     51.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                 Last
                                                                                                                Created)
Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                         Score 379.5;
Pred. No. 2.36
32; Mismatches
                                          Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                F7B078680554BC31 CRC64;
                                                                                                   annotation
                                                                                                                sequence
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                                                                                                               update)
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                                           Spirurida;
                                                                                                 update)
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                                             Filarioidea;
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61 61

LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120 LPSQQPRFILLSWCKKHSDERISYPMLLIYYCPNGSSPELQMLYAGSRNFIVNECHVSKV

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Best Local S
Matches 65
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Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein Y50D7A.10.
Y50D7A.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 186:1-5(1997).

EMBL; U62806; AAC47468.1; ..

InterPro; IPR002108; Actbind_cofln.

Pfam; PF00241; cofilin_ADF; 1.

SMART; SM00102; ADF; 1.
                                                                                                                                                                                                                         Waterston R.; Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC024801; AAN84814.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-Bristol N2; MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-97199361; PubMed-9047337;
Liu L.X., Xu H., Weller P.F., Shi A.,
"Structure and expression of a novel
                                                                                                                                                                                         Hypothetical protein. SEQUENCE 145 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                           STRAIN-Bristol
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Strowmatt C.;
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                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=6239;
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65; Conserv
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                                MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME
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MTSSLTICSIPDGVKEDLKKFRFSKSTTMNALILKIDRESHELQSEQLLNDCSIEEFKEE
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                                                                                           35.5%;
llarity 41.7%;
Conservative 2!
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                                                                                                                                                                                                                                                                                                             N2;
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                                                                                                                                                                                         16992 MW;
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                                                                                                                                                                                                                                                                                                                                                                                cosmid Y50D7A.";
EMBL/GenBank/DDBJ
                                                                                         Score 261; DB
Pred. No. 8.7e
25; Mismatches
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromadorea;
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                                                                                                                                                                                         A39D2293A31CDD1C CRC64;
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filarial gene for glia maturation
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8.7e-18;
hes 45;
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9.9e-29;
hes 36;
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                                                                                                                                     Length 145;
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RESULT 11
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Matches 35
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002
01-OCT-2002
01-MAR-2003
                                              Skelton J., Churcher C.M., Barrell Submit-Led (AUG-1997) to the EMBL/Ge EMBL, 298597; CAB11220.1; -. GeneDB_Spombe; SPAC17H9.11; -. Interpro; IPR002108; Actbind_cofln.
                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Cofilin/tropomyosin-type actin binding protein.
SPAC17H9.11.
                                                                                                                                                                                Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                          SEQUENCE
                                      InterPro;
SMART; SM
                                                                                                                SEQUENCE FROM N.A.
STRAIN=972h-;
                                                                                                                                                                                                                                                                                         013808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AY118642; AAM50011.1; -. FlyBase; FBgn0028894; BG:DS02740.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sD03793p.
BG:DS02740.9 OR BCDNA:SD03793 OR CG5869.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Bucharyota; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                        NCBI_TaxID=4896;
                                                                                                                                                                     Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                      013808
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InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; I.
SEOUENCE 65 AA; 7920 MW; 7F0655F36C38489E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                     62
                                      SM00102;
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35; Conserv
                          141 AA;
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(TrEMBLrel. 22,
(TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                      ADF;
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23.8%;
                          MW;
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                                                                                      Barrell B.G., Rajandream M.A., EMBL/GenBank/DDBJ databases.
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Score 175;
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Pred. No. 9.
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                          96CB544AE4FD9CAD CRC64;
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Length 141;
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                                                      01-DEC-2001 (TrEMBLrel. 01, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 37.5 kDa protein.
 Eukaryota; Metazoa; Rhabditidae; Peloder NCBI_TaxID=6239;
                                                  Hypothetical F38E9.5.
                                                                                                                                                                                                                                                                                                                                                                                                                Murphy L., Harris D., Lyne M., Rajandream M.A., Barrell B.G.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL; ALO34490; CAA22475.1; ... GenebB_SPombe; SPCC126.06; ... InterPro; IPR002108; Actbind_cofin. PR00241; cofilin_ADF; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                    Caenorhabditis elegans
                                                                                                 020173;
01-NOV-1996
                                                                                                                          Q20173
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00102; ADF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-972h-;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                     KIESNDAADITE 296
                                                                                                                                                                                                                                                 PRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQT--AELTKVFE-
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                                                                                                                                                                                                            -IRTTD--DLTE
                                                                                                                                                                                                                                  PNFAFYS---LPKDG--SSKILFIYICPMQATVKHRMVYSSSKLGLLDSIKAELGIVIDG
                                                                                                                                                                                                                                                                                 VAMSIDDKALKALSD--LKSSTENNLVILSIDK--EVISLSQEKQNIPPSDVKSFFSSTE
                                                                                                                                                                                                                                                                                                         VVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQ
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                                                                                                                                                                                                                                                                                                                                                                                 328 AA;
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                          PRELIMINARY;
            Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
            Nematoda; Chromadorea; inae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                               36780 MW;
                                                                                                                                                                                                                                                                                                                                            16.8%;
29.5%;
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                                                                                                                                                                                                            131
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                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                                                                                                                                              Score 123.5; DB 3
Pred. No. 0.00054;
8; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138
                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                               D07F7566404DE5FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ches 63;
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                         Rhabditida;
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                       Rhabditoidea;
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Q12156
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Best Local S
Matches 35
                                              SEQUENCE
Bloecker
                                                                                              Brandt P., Ramlow S., Otto B., Bloecker H.; "Nucleotide sequence analysis of a 32,500 bp of Saccharomyces cerevisiae chromosome IV.";
                                                                                                                                                                                                                  01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-JUN-2002 (TIEMBLIEL 21, Last annotation updat
Hypothetical 17.1 kDa protein YDR063W.
YDR063W OR D4245.
                                                                                                                                                                                                                                                                                Q12156;
Q12156;
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; Saccharom
NCBI_TaxID=4932;
                                  Bloecker H., Brandt
Submitted (JUL-1996)
                                                                                 of Saccharomyces cerevisiae Yeast 12:85-90(1996).
                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=96381250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002108; Actbind_cofln.
Pfam; PF00241; cofilin_ADF; 2.
ProDom; PD002129; Actbind_cofln; 1.
            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00102; ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Direct Submission.";
Submitted (SEP-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Bristol N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol
Gattung S., Wu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U46668; AAA93345.2; WormPep; F38E9.5; CE28307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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AIN=Bristol N2;
tung S., Wu X.;
e sequence of C.
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Similarity 25.4%;
35; Conservative 3
                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    KVFEIRTTDDLTEAWLQE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAFPVDRNAEEALRQLASQK----LSFVQLSVDTLNEAIKLEGTLESLEPSQLASKVPRDK
                                                                                                                                                                                                                                                                                                                                                       NKMEVDARDDLSEKALLE
                                                                                                                                                                                                                                                                                                                                                                                                      PRYTFYNFDHTW-EGVPQQCTLFIYSLPSSGSSIKERMLYSSCKGPFLSAAQNQYGVVIT
                                                                                                                                                                                                                                                                                                                                                                                                                            PREVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE-----LT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JAN-1996)
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333 AA; 37525 MW;
                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                   PubMed=8789263;
                                              P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
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EMBL/GenBank/DDBJ
                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 119.5; DB Pred. No. 0.0014; 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A62F4AF3BAEF98AA CRC64;
                                                                                                                                                                                                                                                                                              149
                                                                                                                                                                                  Saccharomyces
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                                                                                                                                                                                                                                               update)
                                                                                                           region
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                                                                                                                                                                                              Saccharomycetes;
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Best Local :
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                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022344; AAH22344.1; -
InterPro; IPR002108; Actbind_cofln.
SMART; SM00102; ADF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBTCD3 PRELIMINARY; PRT; OBTCD3; O1-JUN-2002 (TrEMBLrel. 21, Created) O1-JUN-2002 (TrEMBLrel. 21, Last seq O1-OCT-2002 (TrEMBLrel. 22, Last ann Protein tyrosine kinase 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barrell B., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 844162; CAA58979.1; -.
EMBL; 274359; CAA98881.1; -.
EMBL; Z49209; CAA89092.1; -.
SGD; S0002470; YDR063W.
SGD; S0002470; YDR063W.
SGD; S0002470; YDR063W.
SMART; SM00102; ADD; 1.
Hypothetical protein.
SMART; SM00102; ADF; 1.
Hypothetical protein.
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Hunt S., Bowman S., Harris D.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Prostate;
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                  132 PKDSARYHFFLYKHSH-EGDYLESIVFIYSMPGYTCSIRERMLYSSCKSRLLEIVERQLQ 190
117 --LTKVFEIRTTDDLTEAWLQEKL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 LIEVSSGLEDDSDVEELREQL 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 VFEIRT--TDDLTEAWLQEKL 138
                                                                                               08
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                                                                                                                                                                                                                                     6 VYCEYDPELTEKLRKFRFRKETDNAAIIMKYDKDRQMYVLEEEFQNISPEELKMELPERQ 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 KIGTETRNKIKKFRISTARTUSIKALSIKIEPKPSYEIIVDEDEQEELDEIEDLSELAEI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 EVDPELTEKLRKFR-FRKETDN-AAIIMKVD-KDRQMVVLEEEFQNISPE-----ELKME 60
                                                                                                                                                                               VAFPISREAFQALEKLNURQLN---YVQLEIDIKNEIIIL----ANTINTELK-DLPKRI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPDNSPRFVLTAYPTTTKDGFKQTPLVLVYWKPMTVVSQEWKMLYAGALEMIREECGTFK 125
                                                                                                                                                                                                                                                                                                                                                                                                                          252 AA; 28823 MW; CCE0A5A82BBE109D CRC64;
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                 15.4%; Score 113; DB 4; Length 252; 26.4%; Pred. No. 0.0043; ative 33; Mismatches 53; Indels
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Last annotation update)
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Search completed: September 23, 2003, 15:11:05 Job time : 101 secs

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Result
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US-09-663-600A-223
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Query Match 100.0%; Score 735; DB 2; Len Best Local Similarity 100.0%; Pred. No. 2.5e-83; Matches 142; Conservative 0; Mismatches 0; II	ESULT 1 S-08-187-186A-2 Sequence 2, Application US/08187186A Patent No. 592572 Sequence 2, Application US/08187186A Patent No. 592572 GENERAL INFORMATION: APPLICANT: Craig A. Rosen; Henrik Olsen; APPLICANT: Mark D. Adams; and Ewen Kirkness TITLE OF INVENTION: HAEMOPOIETIC MATURATION FACTOR NUMBER OF SEQUENCES: APDLESSE: CECCHI, STEWART & OLSTEIN STATES E. CECCHI, STEWART & OLSTEIN STATES: NEW JERSEY COUNTRY: USA ZIP: 07068 COMPUTER: NEW JERSEY COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INCH DISKETTE COMPUTER READABLE WS-DOS SOFTWARE: WORD PERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/187,186A FILING DATE: January 25, 1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: MULLINS, J.G. APPLICATION INFORMATION: REGISTRATION SUMBER: 325800-46 (PF105) TELECOMMUNICATION INFORMATION: TELEPHONE: 201-994-1700 TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 142 AMINO ACIDS TYPE: AMINO ACIDS STRANDEDNESS: TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN TS-08-187-186A-2	ALIGNMENTS	28 71 9.7 1650 4 US-09-535-008-71 29 69 9.4 254 3 US-09-318-448-25 30 69 9.4 428 4 US-09-134-001C-2942 31 69 9.4 793 4 US-09-107-532A-5141 32 68.5 9.3 434 4 US-09-595-424-6 33 68.5 9.3 454 3 US-09-595-424-6 34 68.5 9.3 454 3 US-09-595-124-6 35 68 9.3 454 3 US-08-704-870-5 36 68 9.3 454 3 US-08-0115-5 37 68 9.3 454 6 5260432-2 39 67.5 9.2 887 4 US-09-328-352-4479 40 67.5 9.2 1151 4 US-09-328-352-8876 41 67.5 9.2 1151 4 US-09-328-352-8876 42 66.5 9.0 307 4 US-09-754-60-16 43 66.5 9.0 414 4 US-09-286-981B-10 45 66.5 9.0 564 3 US-09-308-022-6
Length 142; Indels 0;			Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Patent No. Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: LIN
MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 32:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/187,186
FILING DATE: 25 JAN 1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US94/05186
FILING DATE: 10 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KIRKNESS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: Concur CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                              LENGTH:
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STATE: NEW JERSEY
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                                                                 LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV
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      FEIRTTDDLTEAWLQEKLSFFR 142
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Pred. No. 2.5e-83;
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US-09-333-033-2
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LENGTH: 142
TYPE: PRT
ORGANISM: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Applicati
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/4
PRIOR FILING DATE: 1995-05-16
PRIOR APPLICATION NUMBER: 08/1
PRIOR FILING DATE: 1994-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PF105P1D1
CURRENT APPLICATION NUMBER: US/09/333,033
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/187,186

FILING DATE: 25 JANUARY 1994

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 32586

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                       COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                   ZIP: 07068
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: NEW JERSEY
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                                                                                                                                                                                                                                                                                                                           E: CARELLA, BYRNE, BAIN, GILFILLAN
E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
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                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                     KIRKNESS,
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                                                                                                                                                                                                                                                                                                                                                                                         Haemopoietic Maturation Factor
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                                                                                             08/187,186
                                                                                                                                                        PCT/US94/05186
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Pred. No. 2.5e-83;
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INFORMATION FOR

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; SEQ ID NO 229
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-663-600A-229
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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
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                                                                                                                                                 Matches 140;
                                                                                                                                                                                       Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/663,600A CURRENT FILING DATE: 2000-09-15 PRIOR APPLICATION NUMBER: 09/191,997 PRIOR FILING DATE: 1998-11-13
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NO:
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS FILE REFERENCE: 31.US3.CIP
                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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VIFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 AMINO ACIDS
TYPE: AMINO ACID
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TOPOLOGY: LI
                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/0 FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/099,273
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61
               61 LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
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                                                                                       1 MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKME 60
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                                                                     MSDSLVVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFRNISPEELKME
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                                                                                                                                                               Score 723; DB 4;
Pred. No. 7.6e-82;
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US-08-187-186A-5
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US-09-333-033-9
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; LENGTH: 141
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 116;
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA: US/08/187,186A
APPLICATION NUMBER: US/08/187,186A
FILING DATE: January 25, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/442,497
PRIOR FILING DATE: 1995-05-16
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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PRIOR FILING DATE: 1994-01-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Craig A. APPLICANT: Mark D. TITLE OF INVENTION:
                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                          COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                             CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                   ADDRESSEE: CARELLA, BYRNE, ADDRESSEE: CECCHI, STEWART
                                                                                                                                                                                                                                                                                    STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                  Craig A.
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                                                                                                                                                                                                                                                                                                                                                                                               Adams; and
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nd Ewen Kirkness
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& OLSTEIN
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RESULT 8
US-08-442-497C-9
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE 141 AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                             INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 INC
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05186
FILING DATE: 10 MAY 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
             SEQUENCE CHARACTERISTICS:
                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                          TELEPHONE: 201-994-1744
                                                                                           NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
                                                                                                                                                                                   APPLICATION NUMBER: 08/1 FILING DATE: 25 JAN 1994
                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: Concur:
                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                               CLASSIFICATION:
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ZIP: 07068
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LENGTH:
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E: CECCHI, STEWART & OLSTEIN
6 BECKER FARM ROAD
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                                                       201-994-1700
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82.3%;
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Pred. No. 7.8e-69;
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                                                                                   325800-282
                                                                                   (PF105P1)
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US-09-663-600A-213
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; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-442-497C-9
                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR PPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR PPLICATION NUMBER: 60/074,121
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
                                                                                                                                                                                                                                                SOFTWARE: Patent.pm
SEQ ID NO 213
LENGTH: 109
                                                                                                                                    Matches
                                                                                                                                                                 Query Match
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Best Local Similarity
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CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1998-04-13 PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CONAS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/099,273 PRIOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 31.US3.CIP
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TYPE: PRT
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                                                                al Similarity
107; Conserv
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61 VGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTDDLTEAWLQEKLSFFR 109
                                 94 VGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTDDLTEAWLQEKLSFFR 142
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98.2%;
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                                                                                                                                Score 558; DB Pred. No. 1.5e 1; Mismatches
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Pred. No. 2
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2.4e-68;
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.5e-61;
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RESULT 10 US-08-184-252A-2

Sequence 2, Application US/08184252A Patent No. 5573935

GENERAL INFORMATION:

Beeler, John F.

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RESULT 11
US-09-123-851-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOV
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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REFERENCE/COCKET NUMBER: UNITELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
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                                                                COUNTRY: UZIP: 94304
OPERATING SYSTEM:
                 COMPUTER:
                                                                                                           CITY: Palo Alto
                                                                                                                              STREET:
                                                                                                                                               ADDRESSEE:
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38; Conserv
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amino acid
XY: linear
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                                                                                                                              E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
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                                                                            U.S.
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VENTION: PROTEIN TYROSINE KINASE
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          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 113; DB 1; 26.4%; Pred. No. 1.2e-05; tive 33; Mismatches 53;
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US-08-728-520-3
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Sequence 3, Application US/08728520 Patent No. 5994112
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                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                             APPLICATION NUMBER: US/08/728,520 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                      COMPUTER: IBM CONTROL OPERATING SYSTEM:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                 ZIP: 94304
                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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CLONE: 451482
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Billings, Lucy J.
Billings, Lucy J.
36,749
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                                                                                                                                                                                                                                                                                                U.S.
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26.4%;
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PF-0136 US
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TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:

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TELEPHONE:

415-845-4166

TELECOMMUNICATION INFORMATION:

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GENERAL INFORMATION:
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Best Local Similarity
Query Match
Best Local Similarity
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                                                                                                                                                  TELEFAX: (619) 235-01: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                               LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                   NAME: Israelsen, Ned A. REGISTRATION NUMBER: 29,655 REFERENCE/DOCKET NUMBER: NI
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Newport Beach
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620 Newport Center Drive, Sixteenth Floor
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15.4%;
26.4%;
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Score 113; DB 5; Pred. No. 1.2e-05;
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US-09-123-851-4
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US-09-123-851-4
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                                                                                                                                                                                    Query Match
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Patent No. 5958405
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
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TITLE OF INVENTION:
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                                                                                                                                                     Local Similarity
nes 37; Conserv
                                                                                                                                                                                                                               LIBRARY: GenBank CLONE: 1166579
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Billings, Lucy REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/123,851
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                                                                                                                      6 VVCEVDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQ 65
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                            PRYTFYNFDHTW-EGVPQQCTLFIYSLPSSGSSIKERMLYSSCKGPFLSAAQNQYGVVIT 286
                                                           PRFVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE------
                                                                                       VAFPVDRNAEEALRQLASQK---LSFVQLSVDTLNEAIKLEGTLESLEPSQLASKVPRDK 227
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 --LTKVFEIRTTDDLTEAWLQEKL 138
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                                                                                                                                                                     Score 106.5;
Pred. No. 7.0
                                                                                                                                                     Mismatches
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 -TTDDLTEAWLQE 136
                                                                                                                                                                     7.6e-05;
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Search completed: September 23, 2003, 15:13:01 Job time : 31 secs
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; LIBRARY: GenBank
; CLONE: 1166579
US-08-728-520-4
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US-08-728-520-4
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                             Ouery Match 14.5%; Score 106.5; DB 2; Best Local Similarity 22.8%; Pred. No. 7.6e-05; Matches 37; Conservative 30; Mismatches 60;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,5;
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
INPLICATION NUMBER:
FILING DATE:
FILING DATE:
THEODMAINTON.
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: IBM Compatible
TOMPUTER: TOMEN: DOS
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
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                                                                                                                                                                                66 PREVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE----- 116
                                                                       NKFLQKRSNKMFKIREKIFLKRLKNDMEVDARDDLSEKALLE 328
                                                                                                                                                 PRYTFYNEDHTW-EGVPQQCTLFIYSLPSSGSSIKERMLYSSCKGPFLSAAQNQYGVVIT 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide
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                                                                                                          -----TTDDLTEAWLQE 136
                                                                                                                                                                                                                                                                                                                                    Length 357;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                 5
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THIS PACK BLANK (USPRO)

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
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                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/U
2: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
3: /cgn2_6/ptodata/1/pubpaa/U
4: /cgn2_6/ptodata/1/pubpaa/U
5: /cgn2_6/ptodata/1/pubpaa/U
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9: /cgn2_6/ptodata/1/pubpaa/U
9: /cgn2_6/ptodata/1/pubpaa/U
10: /cgn2_6/ptodata/1/pubpaa/U
11: /cgn2_6/ptodata/1/pubpaa/U
13: /cgn2_6/ptodata/1/pubpaa/U
14: /cgn2_6/ptodata/1/pubpaa/U
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11: /cgn2_6/ptodata/1/pubpaa/U
12: /cgn2_6/ptodata/1/pubpaa/U
13: /cgn2_6/ptodata/1/pubpaa/U
14: /cgn2_6/ptodata/1/pubpaa/U
15: /cgn2_6/ptodata/1/pubpaa/U
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735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             September 23, 2003, 15:07:23;
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                                                                                                                                                                                                         Cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PC7_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
SUMMARIES
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(without alignments)
783.069 Million cell updates/sec
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Result	Score	Query Match	Query Match Length DB	DB	ID	Description
μ.	735	100.0	142	14	US-10-004-832-2	Sequence 2. Appli
2	723	98.4	142	12	2 US-10-319-763-229	Sequence 229, App
ω	699	95.1	147	9	US-09-925-302-642	Sequence 642, App
4	614	83.5	141	14	US-10-004-832-9	Sequence 9. Appli
υ	558	75.9	109	12	US-10-319-763-213	Sequence 213, App
σ	113	15.4	350	11	US-09-251-225-3	Sequence 3, Appli
7	113	15.4	350	15	US-10-097-340-266	Sequence 266, App
80	113	15.4	350	15	US-10-205-823-341	Sequence 341, App
9	113	15.4	385	ø	US-09-925-299-966	Sequence 966, App
10	113	15.4	385	11	US-09-925-299-966	Sequence 966, App
11	113	15.4	385	15	US-10-106-698-4598	Sequence 4598, Ap
12	109.5	14.9	224	14	US-10-108-605-277	Sequence 277, App
13	108	14.7	348	10	US-09-969-384-19	Sequence 19, Appl
14	106.5	14.5	357	11	US-09-251-225-4	Sequence 4, Appli
15	103	14.0	343	11	US-09-251-225-1	Sequence 1, Appli

4	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	66.5	67	67	67	67.5	67.5	83	68	68.5	æ	69	69.5	70.5	70.5	71	71.5	74.5	78.5	78.5
9.0	9.0						9.0			9.0	•	•	9.1	9.1	٠		•	9.3	•	•		9.5			٠		10.1	10.7	10.7
581	539	483 .	481	414	413	376	326	307	254	251	168	1713	1169	440	911	148	454	454	189	189	310	685	487	299	1647	722	487	166	166
11	11	11	11	12	11	11	9	12	11	12	9	15	12	11	15	14	11	9	11	11	10	9	11	9	11	15	11	15	15
US-09-298-523B-56	US-09-298-523B-54	US-09-298-523B-10	US-09-298-523B-6		US-09-056-019-35	US-09-056-019-7	132-5	Ļ	US-09-056-019-9	US-10-254-995-4	US-09-945-301-5	US-10-270-333-177	-10 - 24	US-09-910-186A-8	US-10-204-887-123	US-10-108-605-27	US-09-814-604-3	US-09-797-727-2	US-09-764-881-148	US-09-764-891-3897	US-09-925-300-1602	US-09-801-574-6	US-09-298-523B-9	US-09-815-242-10563	US-09-824-574-4	US-10-029-495-5	US-09-298-523B-66	-823-	US-10-205-342-21
•	54,	10	Sequence 6, Appli	10,		Sequence 7, Appli	585,	Ó	Sequence 9, Appli	4.	5, 2	7	20,	Sequence 8, Appli	123	27	Sequence 3, Appli	2, Api	Sequence 148, App	3897,	e 1602,	Sequence 6, Appli	e 9, App	105	Sequence 4, Appli	Sequence 5, Appli	66	Sequence 72, Appl	•

ALIGNMENTS

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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 09/333,033
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/442,497
PRIOR APPLICATION NUMBER: US 08/442,497
PRIOR FILING DATE: 1995-05-16
PRIOR FILING DATE: 1995-05-16
PRIOR FILING DATE: 1994-01-25
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Kirkness et al.
TITLE OF INVENTION: Human Haemopoietic Maturation Factor
FILE REFERENCE: PF105P1D2
                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10004832 Publication No. US20020146408A1
                                                                                                                                                                                                                                                                                                                               LENGTH: 142
TYPE: PRT
121 FEIRTTDDLTEAWLQEKLSFFR 142
                                                                                                                                                                                                                 142;
                                                           61 LPERQPRFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                               61 LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                                                                                   Conservative
                                                                                                                                                                                                             100.0%; Score 735; DB 14; 100.0%; Pred. No. 5.1e-75; tive 0; Mismatches 0;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                   Length 142;
                                                                                                                                                                                                               0;
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121

FEIRTTDDLTEAWLQEKLSFFR 142

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US-09-925-302-642
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                                                                                                                                                                                                                                                                                                         Sequence 642, Application Patent No. US20020044941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 229
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
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                                                       SEQ ID NO 642
                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEO ID NOS: 896
                                                                                                                                                                                                                                FILE REFERENCE: PA104
                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dumas Milne Edwards, Jean-Baptiste
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1998-09-04
                     TYPE: PRT
ORGANISM: Homo sapiens
                                     ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 LPEROPREVVYSYKYVRDDGRVSYPLCFIESSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   al Similarity
140; Conserv
                                       147
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                                                                                                                                                                                                                                                                                                                           Application US/09925302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 723; DB 12;
Pred. No. 1.2e-73;
1; Mismatches 1.
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                                                                                                                                                                                                                                                  Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 142;
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US-10-319-763-213
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                                                                RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/004,832
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 09/33,033
PRIOR FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: US 08/442,497
PRIOR FILING DATE: 1995-05-16
PRIOR APPLICATION NUMBER: US 08/187,186
PRIOR FILING DATE: 1994-01-25
Sequence 213, Application US/10319763 Publication No. US20030144490A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 135
                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kirkness et al.
TITLE OF INVENTION: Human Haemopoletic Maturation
FILE REFERENCE: PF105P1D2
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: NAME/KEY: SITE LOCATION: (103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE LOCATION: (2)
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 141
                                                                                                                                                                                                                                                                                               Local Similarity
nes 115; Conserv
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nes 135; Conserv
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                                                                                                                                                                          61 LPERQPRFIVYSYKYQHDDGRVSYPLCFIFSSPVGCKPEQQMMYAESKNKLVQTAELTKV 120
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                                                                                                                                                                                                                                   PatentIn version 3.1
                                                                                                             FEIRNTEDLTEEWLREKLGFF 141
                                                                                                                             FEIRTTDDLTEAWLQEKLSFF 141
                                                                                                                                                                                                       LPERQPREVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFVVYSYKYVHDDGRVSYPLCFIFSSPVGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTT 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDLTEAWLQEKLSFFR 147
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                                                                                                                                                                                                                                                                                                  Conservative
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99.3%;
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Pred.
                                                                                                                                                                                                                                                                                                             Score 614; DB 14;
Pred. No. 2.2e-61;
                                                                                                                                                                                                                                                                                                  Mismatches
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No. 6.1e-71;
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                                                                                                                                                                                                                                                                                                                               Length 141;
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APPLICANT: Dumas Milne Edwards, Jean-Baptiste APPLICANT: Duclert, Aymeric

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PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09251225 Publication No. US20030099652A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/096,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bougueleret, Lydi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: G-031.US04.DIV
TELEFAX: 415-845-4166
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 109
                                                                                               APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                         REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                       APPLICATION NUMBER: US/09/251,225 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: GOLI, SUTYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE NUMBER OF SEQUENCES: 4
CORDEGEOCUTOTION: -----
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                     94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKVDKDRQMVVLEEEFRNISPEELKMELPERQPRFVVYSYKYVRDDGRVSYPLCFIFSSP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGCKPEQQMMYAGSKNRLVQTAELTKVFEIRTTDDLTEAWLQEKLSFFR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                              CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.
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98.2%;
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                                                                                  PF-0136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 558; DB 12;
Pred. No. 3.2e-55;
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                                                                                  SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12;
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US-10-097-340-266
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SOFTWARE: Fast
SEQ ID NO 266
SEQ TENGTH: 350
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Matches
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                                                                                                                                                                                                         TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-25,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR APPLICATION NUMBER: 60/325,026
PRIOR APPLICATION NUMBER: 60/326,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/374,967
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
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                                                                     NUMBER OF SEQ ID NOS:
                                                                                      PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19
                                                                                                                             PRIOR APPLICATION NUMBER: 60/325,102 PRIOR FILING DATE: 2001-09-26
                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/311,732 PRIOR FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: pept:
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 26.4 nes 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 P----REVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE----
                                             FastSEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karen GLATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xumei ZHAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steve G. KOVATS
Rachel E. MEYERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shubhangi KAMATKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sebastian HOERSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michael MORRISEY
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                                               for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 341
LENGTH: 350
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/205,823 CURRENT FILING DATE: 2002-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
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                         117
                                                                                                                                               178 VAFPISREAFQALEKLNNRQLN---YVQLEIDIKNEIIIL----ANTTNTELK-DLPKRI 229
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                                                               PKDSARYHFFLYKHSH-EGDYLESIVFIYSMPGYTCSIRERMLYSSCKSRLLEIVERQLQ 288
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                     --LTKVFEIRTTDDLTEAWLQEKL 138
                                                                                                       P----RFVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE---- 116
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Gorbatcheva, Bella
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Kamatkar, Shubhangi
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                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                             15.4%; Score 113; DB 15; 26.4%; Pred. No. 0.00021; tive 33; Mismatches 53;
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US-09-925-299-966
US-09-925-299-966, Application US/09925299
; Publication No. US20030040617A9
; Publication No. US20030040617A9
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SEQ ID NO 966
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 966 LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
Query Match
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NO FILE REFERENCE: PA102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA102 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rosen et al.
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NAME/KEY: SITE
LOCATION: (221)
                                                                                                                                           TYPE: PRT
ORGANISM: Homo
                                                               OTHER INFORMATION:
                                                                                NAME/KEY: SITE LOCATION: (221
                                                                                                                            FEATURE:
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les 38; Conserv
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                                                                                    (221)
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Pred. No. 0.00024;
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  Score 113;
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                                                             of the naturally occurring L-amino
  DB 11;
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Gaps

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RESULT 12
US-10-108-605-277
; Sequence 277, Application US/10108605
; Publication No. US20020160934A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PRIOR FILING DATE: 1999-11-03; NUMBER OF SEQ ID NOS: 8564; SOFTWARE: PATENTIN Ver. 3.0; SEQ ID NO 4598; LENGTH: 385; TYPE: PRT
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                                                                                                GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
               APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
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       FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
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NAME/KEY: MISC_FEATURE
LOCATION: (221)
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38; Conser
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                                                                                              Stam, Lynn
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3; Mismatches 53;
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RESULT 14
US-09-251-225-4
; Sequence 4, Application US/09251225
; Publication No. US20030099652A1
; GENERAL INFORMATION:
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Best Local
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; ORGANISM: Drosophila melanogaster US-10-108-605-277
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 277
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19, Application US/09969384
Publication No. US20020192749A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Moore, et al. TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT055P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/10542
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/236, 384
PRIOR FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/969,384 CURRENT FILING DATE: 2001-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 09/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/176,418
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/194,118
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                         181 LQPEAQRALQQL---KQKMVNYIQMKLDLERETI----ELVHTEPTDV-AQLPSRVPRDA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 SVRERMMYSSCKAPFLDELAALGVEVVKKLEIDSGSELTEAFLQDEL 192
                                                                                                                                                                                                               10 VDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 KPEQQMMYAGSKNRLVQT-----AELTKVFEIRTTDDLTEAWLQEKL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 LEEEQIHVSRAAKVELADLPKQVPEDHARYHLFLFRHTHEGDYFESY--VFVYSMPGYSC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 LEEEFQNISP-----EELKMELPERQPRFVVYSYKYVHD-DGRVSYPLCFIFSSP-VGC
                                                                                                                                                                                                                                                                  1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Ver. 2.0
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KKIEIGDGAELTGEFLYDEV 311
                                         KVFEIRTTDDLTEAWLQEKL 138
                                                                                      ARYHFFLYKHTH-EGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIA 291
                                                                                                                             -RFVVYSYKYVHDDGRVSYPLCF1FSSP-VGCKPEQQMMYAGSKNRLVQTA-----ELT 118
                                                                                                                                                                                                                                                                  Conservative
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29.9%;
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                                                                                                                                                                                                                                                                                    Score 108; DB 10;
Pred. No. 0.00078;
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Pred. No. 0.00029;
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                                                                                                                                                                                                                                                                                                         Length 348;
                                                                                                                                                                                                                                                                Indels
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APPLICANT: GOli, Surya K. TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS

ADDRESSEE:

Incyte Pharmaceuticals, Inc

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RESULT 15
US-09-251-225-1
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                                                                                                                                                                     Sequence 1, Application US/09251225
Publication No. US20030099652A1
GENERAL INFORMATION:
APPLICANT: Goll, Surya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,2
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 415-855-0555
TELEFAX: ;415-845-4166
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                            APPLICANT: GO11, SUTYA K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1166579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 31, -
                                               CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                 94304
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                                                                                                                                                                                                                                                                                                       NKFLQKRSNKMFKIREKIFLKRLKNDMEVDARDDLSEKALLE 328
                                                                                                                                                                                                                                                                                                                                                                                                         PRFVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTAE------
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                                   U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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В
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                                                                                                                                                                                                                                       Query Match 14.0%; Score 103; DB 11; Length 343; Best Local Similarity 26.4%; Pred. No. 0.0028; Matches 37; Conservative 32; Mismatches 51; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Billings, Lucy J.
REGISTION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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Consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/251,225 FILING DATE: Filed Herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                                                                                                           182 LQPEAQRALQQL---KQKMVNYIQMKLDLERETI----ELVHTEPTDV-AQLPFRVPRDA 233
293 KKIEIGDGAELTAEFLYDEV 312
                                                                             234 ARYHXFLYKHNH-EGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIA 292
                                                                                                                     67
                                                                                                                                                                                     10 VDPELTEKLRKFRFRKETDNAAIIMKVDKDRQMVVLEEEFQNISPEELKMELPERQP--- 66 : | | : : : | | | |
                                                                                                             -RFVVYSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQQMMYAGSKNRLVQTA-----ELT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                   KVFEIRTTDDLTEAWLQEKL 138
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Gaps

Search completed: September 23, 2003, 15:12:24 Job time : 28 secs